



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/767,308

DATE: 08/04/2004

TIME: 08:44:13

Input Set : N:\Cr3\RULE60\10767308.raw

Output Set: N:\CRF4\08042004\J767308.raw

1 <110> APPLICANT: Kapeller Libermann, Rosana  
 2 White, David  
 3 MacBeth, Kyle J.  
 4 <120> TITLE OF INVENTION: 2786, A NOVEL HUMAN AMINOPEPTIDASE  
 5 <130> FILE REFERENCE: 5800-62  
 6 <140> CURRENT APPLICATION NUMBER: US/10/767,308  
 7 <141> CURRENT FILING DATE: 2004-01-29  
 8 <150> PRIOR APPLICATION NUMBER: US/09/443,795  
 9 <151> PRIOR FILING DATE: 1999-11-19  
 10 <160> NUMBER OF SEQ ID NOS: 2  
 11 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 650  
 15 <212> TYPE: PRT  
 16 <213> ORGANISM: Homo sapiens  
 17 <400> SEQUENCE: 1

18	Met	Ala	Ser	Gly	Glu	His	Ser	Pro	Gly	Ser	Gly	Ala	Ala	Arg	Arg	Pro
19	1			5						10				15		
20	Leu	His	Ser	Ala	Gln	Ala	Val	Asp	Val	Ala	Ser	Ala	Ser	Asn	Phe	Arg
21				20					25					30		
22	Ala	Phe	Glu	Leu	Leu	His	Leu	His	Leu	Asp	Leu	Arg	Ala	Glu	Phe	Gly
23				35				40					45			
24	Pro	Pro	Gly	Pro	Gly	Ala	Gly	Ser	Arg	Gly	Leu	Ser	Gly	Thr	Ala	Val
25				50				55				60				
26	Leu	Asp	Leu	Arg	Cys	Leu	Glu	Pro	Glu	Gly	Ala	Ala	Glu	Leu	Arg	Leu
27	65					70				75				80		
28	Asp	Ser	His	Pro	Cys	Leu	Glu	Val	Thr	Ala	Ala	Ala	Leu	Arg	Arg	Glu
29					85					90				95		
30	Arg	Pro	Gly	Ser	Glu	Glu	Pro	Pro	Ala	Glu	Pro	Val	Ser	Phe	Tyr	Thr
31				100					105					110		
32	Gln	Pro	Phe	Ser	His	Tyr	Gly	Gln	Ala	Leu	Cys	Val	Ser	Phe	Pro	Gln
33				115				120					125			
34	Pro	Cys	Arg	Ala	Ala	Glu	Arg	Leu	Gln	Val	Leu	Leu	Thr	Tyr	Arg	Val
35				130				135				140				
36	Gly	Glu	Gly	Pro	Gly	Val	Cys	Trp	Leu	Ala	Pro	Glu	Gln	Thr	Ala	Gly
37	145					150				155				160		
38	Lys	Lys	Lys	Pro	Phe	Val	Tyr	Thr	Gln	Gly	Gln	Ala	Val	Leu	Asn	Arg
39					165					170				175		
40	Ala	Phe	Phe	Pro	Cys	Phe	Asp	Thr	Pro	Ala	Val	Lys	Tyr	Lys	Tyr	Ser
41				180					185					190		
42	Ala	Leu	Ile	Glu	Val	Pro	Asp	Gly	Phe	Thr	Ala	Val	Met	Ser	Ala	Ser
43				195				200					205			
44	Thr	Trp	Glu	Lys	Arg	Gly	Pro	Asn	Lys	Phe	Phe	Phe	Gln	Met	Cys	Gln

ENTERED

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45	210	215	220
46	Pro Ile Pro Ser Tyr Leu	Ile Ala Leu Ala Ile	Gly Asp Leu Val Ser
47	225	230	235
48	Ala Glu Val Gly Pro Arg Ser Arg Val	Trp Ala Glu Pro Cys Leu Ile	
49	245	250	255
50	Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val	Ile Glu Glu Phe Leu Ala	
51	260	265	270
52	Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val	Trp Gly Arg Tyr Asp Leu	
53	275	280	285
54	Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys		
55	290	295	300
56	Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala		
57	305	310	315
58	Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val		
59	325	330	335
60	Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met		
61	340	345	350
62	Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr		
63	355	360	365
64	Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp		
65	370	375	380
66	Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu		
67	385	390	395
68	Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys		
69	405	410	415
70	Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp		
71	420	425	430
72	Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg		
73	435	440	445
74	Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro		
75	450	455	460
76	Glu Leu Lys Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp		
77	465	470	475
78	Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser		
79	485	490	495
80	Pro Gly Asp Ser Leu Met Lys Pro Ala Glu Glu Leu Ala Gln Leu Trp		
81	500	505	510
82	Ala Ala Glu Glu Leu Asp Met Lys Ala Ile Glu Ala Val Ala Ile Ser		
83	515	520	525
84	Pro Trp Lys Thr Tyr Gln Leu Val Tyr Phe Leu Asp Lys Ile Leu Gln		
85	530	535	540
86	Lys Ser Pro Leu Pro Pro Gly Asn Val Lys Lys Leu Gly Asp Thr Tyr		
87	545	550	555
88	Pro Ser Ile Ser Asn Ala Arg Asn Ala Glu Leu Arg Leu Arg Trp Gly		
89	565	570	575
90	Gln Ile Val Leu Lys Asn Asp His Gln Glu Asp Phe Trp Lys Val Lys		
91	580	585	590
92	Glu Phe Leu His Asn Gln Gly Lys Gln Lys Tyr Thr Leu Pro Leu Tyr		
93	595	600	605

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```

94      His Ala Met Met Gly Gly Ser Glu Val Ala Gln Thr Leu Ala Lys Glu
95          610                      615                      620
96      Thr Phe Ala Ser Thr Ala Ser Gln Leu His Ser Asn Val Val Asn Tyr
97      625                      630                      635                      640
98      Val Gln Gln Ile Val Ala Pro Lys Gly Ser
99          645                      650
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 2459
103 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
105 <220> FEATURE:
106 <221> NAME/KEY: CDS
107 <222> LOCATION: (62)...(2011)
108 <400> SEQUENCE: 2
109      gcgccgcgct cgacctcccc tcgggttcgc ggcccggccg gtgagcaacg gctctgcggc      60
110      c atg gcg agc ggc gag cat tcc ccc ggc agc ggc gcg gcc cgg cgg ccg      109
111      Met Ala Ser Gly Glu His Ser Pro Gly Ser Gly Ala Ala Arg Arg Pro
112      1          5          10          15
113      ctg cac tcc gcg cag gct gtg gac gtg gcc tcg gcc tcc aac ttc cgg      157
114      Leu His Ser Ala Gln Ala Val Asp Val Ala Ser Ala Ser Asn Phe Arg
115          20          25          30
116      gcc ttt gag ctg ctg cac ttg cac ctg gac ctg cgg gct gag ttc ggg      205
117      Ala Phe Glu Leu Leu His Leu His Leu Asp Leu Arg Ala Glu Phe Gly
118          35          40          45
119      cct cca ggg ccc ggc gca ggg agc cgg ggg ctg agc ggc acc gcg gtc      253
120      Pro Pro Gly Pro Gly Ala Gly Ser Arg Gly Leu Ser Gly Thr Ala Val
121      50          55          60
122      ctg gac ctg cgc tgc ctg gag ccc gag ggc gcc gcc gag ctg cgg ctg      301
123      Leu Asp Leu Arg Cys Leu Glu Pro Glu Gly Ala Ala Glu Leu Arg Leu
124      65          70          75          80
125      gac tcg cac ccg tgc ctg gag gtg acg gcg gcg gcg ctg cgg cgg gag      349
126      Asp Ser His Pro Cys Leu Glu Val Thr Ala Ala Ala Leu Arg Arg Glu
127          85          90          95
128      cgg ccc ggc tcg gag gag ccg cct gcg gag ccc gtg agc ttc tac acg      397
129      Arg Pro Gly Ser Glu Glu Pro Pro Ala Glu Pro Val Ser Phe Tyr Thr
130          100          105          110
131      cag ccc ttc tcg cac tat ggc cag gcc ctg tgc gtg tcc ttc ccg cag      445
132      Gln Pro Phe Ser His Tyr Gly Gln Ala Leu Cys Val Ser Phe Pro Gln
133          115          120          125
134      ccc tgc cgc gcc gcc gag cgc ctc cag gtg ctg ctc acc tac cgc gtc      493
135      Pro Cys Arg Ala Ala Glu Arg Leu Gln Val Leu Leu Thr Tyr Arg Val
136      130          135          140
137      ggg gag gga ccc ggg gtt tgc tgg ttg gct ccc gag cag aca gca gga      541
138      Gly Glu Gly Pro Gly Val Cys Trp Leu Ala Pro Glu Gln Thr Ala Gly
139      145          150          155          160
140      aag aag aag ccc ttc gtg tac acc cag ggc cag gct gtc cta aac cgg      589
141      Lys Lys Lys Pro Phe Val Tyr Thr Gln Gly Gln Ala Val Leu Asn Arg
142          165          170          175
143      gcc ttc ttc cct tgc ttc gac acg cct gct gtt aaa tac aag tat tca      637

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144	Ala Phe Phe Pro Cys Phe Asp Thr Pro Ala Val Lys Tyr Lys Tyr Ser	
145	180 185 190	
146	gct ctt att gag gtc cca gat ggc ttc aca gct gtg atg agt gct agc	685
147	Ala Leu Ile Glu Val Pro Asp Gly Phe Thr Ala Val Met Ser Ala Ser	
148	195 200 205	
149	acc tgg gag aag aga ggt cca aat aag ttc ttc ttc cag atg tgt cag	733
150	Thr Trp Glu Lys Arg Gly Pro Asn Lys Phe Phe Phe Gln Met Cys Gln	
151	210 215 220	
152	ccc atc ccc tcc tat ctg ata gct ttg gcc atc gga gat ctg gtt tgc	781
153	Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser	
154	225 230 235 240	
155	gct gaa gtt gga ccc agg agc cgg gtg tgg gct gag ccc tgc ctg att	829
156	Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile	
157	245 250 255	
158	gat gct gcc aat gag gag tac aac ggg gtg ata gaa gaa ttt ttg gca	877
159	Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val Ile Glu Glu Phe Leu Ala	
160	260 265 270	
161	aca gga gag aag ctt ttt gga cct tat gtt tgg gga agg tat gac ttg	925
162	Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu	
163	275 280 285	
164	ctc ttc atg cca ccg tcc ttt cca ttt gga gga atg gag aac cct tgt	973
165	Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys	
166	290 295 300	
167	ctg acc ttt gtc acc ccc tgc ctg cta gct ggg gac cgc tcc ttg gca	1021
168	Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala	
169	305 310 315 320	
170	gat gtc atc atc cat gag atc tcc cac agt tgg ttt ggg aac ctg gtc	1069
171	Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val	
172	325 330 335	
173	acc aac gcc aac tgg ggt gaa ttc tgg ctc aat gaa ggt ttc acc atg	1117
174	Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met	
175	340 345 350	
176	tac gcc cag agg agg atc tcc acc atc ctc ttt ggc gct gcg tac acc	1165
177	Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr	
178	355 360 365	
179	tgc ttg gag gct gca acg ggg cgg gct ctg ctg cgt caa cac atg gac	1213
180	Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp	
181	370 375 380	
182	atc act gga gag gaa aac cca ctc aac aag ctc cgc gtg aag att gaa	1261
183	Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu	
184	385 390 395 400	
185	cca ggc gtt gac ccg gac gac acc tat aat gag acc ccc tac gag aaa	1309
186	Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys	
187	405 410 415	
188	ggg ttc tgc ttt gtc tca tac ctg gcc cac ttg gtg ggt gat cag gat	1357
189	Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp	
190	420 425 430	
191	cag ttt gac agt ttt ctc aag gcc tat gtg cat gaa ttc aaa ttc cga	1405
192	Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg	

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193				435				440				445					
194	agc	atc	tta	gcc	gat	gac	ttt	ctg	gac	ttc	tac	ttg	gaa	tat	ttc	cct	1453
195	Ser	Ile	Leu	Ala	Asp	Asp	Phe	Leu	Asp	Phe	Tyr	Leu	Glu	Tyr	Phe	Pro	
196				450				455				460					
197	gag	ctt	aag	aaa	aag	aga	gtg	gat	atc	att	cca	ggg	ttt	gag	ttt	gat	1501
198	Glu	Leu	Lys	Lys	Lys	Arg	Val	Asp	Ile	Ile	Pro	Gly	Phe	Glu	Phe	Asp	
199	465						470				475					480	
200	cga	tgg	ctg	aat	acc	ccc	ggc	tgg	ccc	ccg	tac	ctc	cct	gat	ctc	tcc	1549
201	Arg	Trp	Leu	Asn	Thr	Pro	Gly	Trp	Pro	Pro	Tyr	Leu	Pro	Asp	Leu	Ser	
202					485					490					495		
203	cct	ggg	gac	tca	ctc	atg	aag	cct	gct	gaa	gag	cta	gcc	caa	ctg	tgg	1597
204	Pro	Gly	Asp	Ser	Leu	Met	Lys	Pro	Ala	Glu	Glu	Leu	Ala	Gln	Leu	Trp	
205				500					505					510			
206	gca	gcc	gag	gag	ctg	gac	atg	aag	gcc	att	gaa	gcc	gtg	gcc	atc	tct	1645
207	Ala	Ala	Glu	Glu	Leu	Asp	Met	Lys	Ala	Ile	Glu	Ala	Val	Ala	Ile	Ser	
208			515					520				525					
209	ccc	tgg	aag	acc	tac	cag	ctg	gtc	tac	ttc	ctg	gat	aag	atc	ctc	cag	1693
210	Pro	Trp	Lys	Thr	Tyr	Gln	Leu	Val	Tyr	Phe	Leu	Asp	Lys	Ile	Leu	Gln	
211	530						535				540						
212	aaa	tcc	cct	ctc	cct	cct	ggg	aat	gtg	aaa	aaa	ctt	gga	gac	aca	tac	1741
213	Lys	Ser	Pro	Leu	Pro	Pro	Gly	Asn	Val	Lys	Lys	Leu	Gly	Asp	Thr	Tyr	
214	545					550				555						560	
215	cca	agt	atc	tca	aat	gcc	cgg	aat	gca	gag	ctc	cgg	ctg	cga	tgg	ggc	1789
216	Pro	Ser	Ile	Ser	Asn	Ala	Arg	Asn	Ala	Glu	Leu	Arg	Leu	Arg	Trp	Gly	
217				565					570					575			
218	caa	atc	gtc	ctt	aag	aac	gac	cac	cag	gaa	gat	ttc	tgg	aaa	gtg	aag	1837
219	Gln	Ile	Val	Leu	Lys	Asn	Asp	His	Gln	Glu	Asp	Phe	Trp	Lys	Val	Lys	
220			580					585					590				
221	gag	ttc	ctg	cat	aac	cag	ggg	aag	cag	aag	tat	aca	ctt	ccg	ctg	tac	1885
222	Glu	Phe	Leu	His	Asn	Gln	Gly	Lys	Gln	Lys	Tyr	Thr	Leu	Pro	Leu	Tyr	
223			595				600					605					
224	cac	gca	atg	atg	ggg	ggc	agt	gag	gtg	gcc	cag	acc	ctc	gcc	aag	gag	1933
225	His	Ala	Met	Met	Gly	Gly	Ser	Glu	Val	Ala	Gln	Thr	Leu	Ala	Lys	Glu	
226		610				615				620							
227	act	ttt	gca	tcc	acc	gcc	tcc	cag	ctc	cac	agc	aat	gtt	gtc	aac	tat	1981
228	Thr	Phe	Ala	Ser	Thr	Ala	Ser	Gln	Leu	His	Ser	Asn	Val	Val	Asn	Tyr	
229	625					630											

**VERIFICATION SUMMARY**

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